Amendments to the Claims

This listing of claims will replace all prior versions, and listings of claims in the application.

1-18. (Cancelled).

19. (Previously presented) A calibrator for absolute quantitation of target RNA by RT-PCR comprising a single cRNA species synthesized by reverse transcription from a synthetic oligonucleotide and quantitatively assayed by an independent method, wherein said synthetic oligonucleotide comprises an amplicon and a promoter sequence located 3' relative to the amplicon.

20. (Previously presented) The calibrator of claim 19, wherein said promoter sequence is a bacteriophage promoter sequence.

21. (Previously presented) The calibrator of claim 20, wherein said promoter sequence is a T7 promoter sequence.

22. (Previously presented) The calibrator of claim 21, wherein said T7 promoter sequence is CCTATAGTGAGTCGTATTA (SEQ ID NO:1).

23. (Previously presented) The calibrator of claim 19, wherein said synthetic oligonucleotide further comprises a flanking sequence of 2-20 nucleotides adjacent to the amplicon.

24. (Previously presented) The calibrator of claim 23, wherein said flanking sequence is 5' and adjacent to the amplicon.

25. (Previously presented) The calibrator of claim 23, wherein said flanking sequence is 3' and adjacent to the amplicon.

26. (Previously presented) The calibrator of claim 23, wherein synthetic oligonucleotide further comprises both a 5' and a 3' flanking sequence adjacent to the amplicon.

27. (Previously presented) The calibrator of claim 23, wherein said flanking sequence is 8 to 12 nucleotides in length.

28. (Previously presented) The calibrator of claim 19, wherein said amplicon is 30 to 70 nucleotides in length.

29. (Previously presented) The calibrator of claim 28, wherein said amplicon is 40 to 60 nucleotides in length.

30. (Previously presented) The calibrator of claim 19, wherein said synthetic oligonucleotide is 60 to 140 nucleotides in length.

31. (Previously presented) The calibrator of claim 30, wherein said synthetic oligonucleotide is 70 to 130 nucleotides in length.

32. (Previously presented) The calibrator of claim 31, wherein said synthetic oligonucleotide is 80 to 120 nucleotides in length.

33. (Previously presented) The calibrator of claim 32, wherein said synthetic oligonucleotide is 90 to 110 nucleotides in length.

34. (Previously presented) The calibrator of claim 19, further comprising heterologous RNA.

35. (Previously presented) The calibrator of claim 34, wherein said heterologous RNA is total RNA.

36. (Previously presented) The calibrator of claim 35, wherein said heterologous RNA is yeast total RNA.

37. (Previously presented) The calibrator of claim 19, wherein said cRNA species is MGB.

38. (Previously presented) The calibrator of claim 19, wherein said cRNA is assayed quantitatively by measuring its absorbance at 260 nm.

39. (Previously presented) A kit comprising the calibrator of claim 19.

40. (Previously presented) The kit of claim 39 comprising more than one aliquot of said cRNA species.

41. (Previously presented) The kit of claim 40, wherein each said aliquot comprises successive serial 1:10 dilutions of said cRNA species.

42. (New) A method for generating calibration data for absolute quantitation of RNA by RT-PCR, the method comprising: (a) providing a chemically-synthesized oligonucleotide comprising an amplicon and a promoter sequence located 3' relative to the amplicon; (b) synthesizing complementary RNA (cRNA) by *in vitro* transcription of the oligonucleotide; (c) quantitating the cRNA; and (d) generating PCR calibration data by performing RT-PCR using a known quantity of the cRNA.

43. (New) The method of claim 42, wherein the promoter sequence is a bacteriophage promoter sequence.

44. (New) The method of claim 43, wherein the bacteriophage promoter sequence is a T7 promoter sequence.

45. (New) The method of claim 44, wherein the T7 promoter sequence consists essentially of 5' CCTATAGTGAGTCGTATTA 3' (SEQ ID NO:1).

46. (New) The method of claim 42, further comprising a 5' flanking sequence consisting of 2 to 20 nucleotides adjacent to the amplicon.

47. (New) The method of claim 46, wherein the 5' flanking sequence consists of 8 to 12 nucleotides.

48. (New) The method of claim 46, wherein the 5' flanking sequence comprises a poly T tail.

49. (New) The method of claim 42, wherein the chemically-synthesized oligonucleotide further comprises a 3' flanking sequence consisting of 2 to 20 nucleotides between the amplicon and the promoter sequence.

50. (New) The method of claim 49, wherein the 3' flanking sequence consists of 8 to 12 nucleotides.

51. (New) The method of claim 42, wherein the length of the amplicon is 30 to 70 nucleotides.

52. (New) The method of claim 51, wherein the length of the amplicon is 40 to 60 nucleotides.

53. (New) The method of claim 42, where in the length of the chemically-synthesized oligonucleotide is 60 to 140 nucleotides.

54. (New) The method of claim 53, wherein the length of the chemically-synthesized oligonucleotide is 70 to 130 nucleotides.

55. (New) The method of claim 54, wherein the length of the chemically-synthesized oligonucleotide is 80 to 120 nucleotides.

56. (New) The method of claim 55, wherein the length of the chemically-synthesized oligonucleotide is 90 to 110 nucleotides.

57. (New) A method for determining the abundance of nucleic acid molecules comprising an amplicon in a test sample, the method comprising: (a) providing a chemically-synthesized oligonucleotide comprising an amplicon and a promoter sequence located 3' relative to the amplicon; (b) synthesizing cRNA by *in vitro* transcription of the oligonucleotide; (c) producing a dilution series using the cRNA; (d) synthesizing single stranded cDNA by reverse transcription of the cRNA; (e) generating PCR calibration data; (f) obtaining RT-PCR test sample data from the test sample; and (g) comparing the PCR test sample data to the PCR calibration data.

58. (New) The method of claim 57, further comprising quantitating the cRNA.

59. (New) The method of claim 58, further comprising mixing the cRNA with heterologous RNA before synthesizing the single stranded cDNA.